

R. Hutson

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05/07/01

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/502,498

DATE: 11/28/2000
 TIME: 14:54:34

Input Set : A:\09502498.txt
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3 <110> APPLICANT: Kilian, Andrzej
 4 Bowtell, David
 7 <120> TITLE OF INVENTION: VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES
 8 THEREOF
 10 <130> FILE REFERENCE: 190106.407
 12 <140> CURRENT APPLICATION NUMBER: 09/502,498
 13 <141> CURRENT FILING DATE: 2000-02-11
 15 <150> PRIOR APPLICATION NUMBER: US 09/108,401
 16 <151> PRIOR FILING DATE: 1998-06-30
 18 <160> NUMBER OF SEQ ID NOS: 155
 20 <170> SOFTWARE: PatentIn Ver. 2.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 3964
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
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92 gtgtgccctg tacacaggcg aggacctgc acctggatgg gggtcctgt gggtaaaat 3900
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96 <210> SEQ ID NO: 2

97 <211> LENGTH: 1132

98 <212> TYPE: PRT

99 <213> ORGANISM: Homo sapiens

101 <400> SEQUENCE: 2

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105 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
106 20 25 30
108 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
109 35 40 45
111 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
112 50 55 60

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114 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
115 65 70 75 80
117 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
118 85 90 95
120 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
121 100 105 110
123 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
124 115 120 125
126 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val
127 130 135 140
129 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
130 145 150 155 160
132 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
133 165 170 175
135 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
136 180 185 190
138 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
139 195 200 205
141 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
142 210 215 220
144 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
145 225 230 235 240
147 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
148 245 250 255
150 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
151 260 265 270
153 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
154 275 280 285
156 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
157 290 295 300
159 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
160 305 310 315 320
162 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
163 325 330 335
165 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
166 340 345 350
168 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
169 355 360 365
171 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
172 370 375 380
174 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
175 385 390 395 400
177 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
178 405 410 415
180 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
181 420 425 430
183 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
184 435 440 445
186 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe

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187      450      455      460
189 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
190 465      470      475      480
192 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
193      485      490      495
195 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
196      500      505      510
198 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
199      515      520      525
201 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
202      530      535      540
204 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
205 545      550      555      560
207 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
208      565      570      575
210 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
211      580      585      590
213 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
214      595      600      605
216 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
217      610      615      620
219 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
220 625      630      635      640
222 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
223      645      650      655
225 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
226      660      665      670
228 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
229      675      680      685
231 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
232      690      695      700
234 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
235 705      710      715      720
237 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
238      725      730      735
240 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
241      740      745      750
243 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
244      755      760      765
246 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
247      770      775      780
249 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
250 785      790      795      800
252 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
253      805      810      815
255 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
256      820      825      830
258 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
259      835      840      845

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261 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
262      850      855      860
264 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
265 865      870      875      880
267 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
268      885      890      895
270 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
271      900      905      910
273 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
274      915      920      925
276 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
277      930      935      940
279 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
280 945      950      955      960
282 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
283      965      970      975
285 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
286      980      985      990
288 Ser Leu Glu Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Gln
289      995      1000      1005
291 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
292      1010      1015      1020
294 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
295 1025      1030      1035      1040
297 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
298      1045      1050      1055
300 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
301      1060      1065      1070
303 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
304      1075      1080      1085
306 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
307      1090      1095      1100
309 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
310 1105      1110      1115      1120
312 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
313      1125      1130
316 <210> SEQ ID NO: 3
317 <211> LENGTH: 1031
318 <212> TYPE: PRT
319 <213> ORGANISM: Emplotes aediculatus
321 <400> SEQUENCE: 3
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326      20      25      30
328 Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
329      35      40      45
331 Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
332      50      55      60

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Input Set : A:\09502498.txt
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L:1360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:3368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:9331 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91
L:9368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:93
L:9410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95